



City Research Online

City, University of London Institutional Repository

Citation: Cowell, R. (2013). A simple greedy algorithm for reconstructing pedigrees. Theoretical Population Biology, 83, pp. 55-63. doi: 10.1016/j.tpb.2012.11.002

This is the accepted version of the paper.

This version of the publication may differ from the final published version.

Permanent repository link: <https://openaccess.city.ac.uk/id/eprint/6011/>

Link to published version: <http://dx.doi.org/10.1016/j.tpb.2012.11.002>

Copyright: City Research Online aims to make research outputs of City, University of London available to a wider audience. Copyright and Moral Rights remain with the author(s) and/or copyright holders. URLs from City Research Online may be freely distributed and linked to.

Reuse: Copies of full items can be used for personal research or study, educational, or not-for-profit purposes without prior permission or charge. Provided that the authors, title and full bibliographic details are credited, a hyperlink and/or URL is given for the original metadata page and the content is not changed in any way.

A simple greedy algorithm for reconstructing pedigrees

Robert G. Cowell^{*,a}

^a*Faculty of Actuarial Science and Insurance, Cass Business School, 106 Bunhill Row,
London EC1Y 8TZ, UK*

Abstract

This paper introduces a simple greedy-search algorithm for finding high-likelihood pedigrees using micro-satellite (STR) genotype information on a complete sample of related individuals. The core idea behind the algorithm is not new, but it is believed that putting it into a greedy search setting, and specifically the application to pedigree learning, is novel. The algorithm does not exploit age or sex information, but this information can be incorporated if desired. Prior information concerning pedigree structure is readily incorporated *after* the greedy-search is completed, on the high-likelihood pedigrees found. The algorithm is applied to human and non-human genetic data and in a simulation study.

Key words:

Pedigree reconstruction, maximum likelihood pedigree, greedy search.

1. Introduction

The reconstruction or estimation of pedigrees of individuals finds applications in both human and non-human populations, for reviews see (Jones and Ardren, 2003; Blouin, 2003; Pemberton, 2008). This paper considers the statistical estimation of pedigrees using genotype markers for a *complete sample* of individuals. Maximum likelihood pedigree estimation was developed by Thompson (1976, 1986) using age and sex information. Almudevar (2003) proposed a simulated annealing approach that avoids the need for age and sex information. Cowell (2009) adapted the Bayesian network learning algorithm of Silander and Myllymäkki (2006) to develop an exhaustive search algorithm that is guaranteed to find a pedigree of highest likelihood; the algorithm has complexity $O(n^3 2^n)$ in the number n of individuals, but is computationally feasible for up to around 30 individuals. A constraint-based integer programming approach is presented in (Cussens, 2010; Cussens et al., 2012) that can find maximum likelihood pedigrees involving more than 30 individuals, giving examples of pedigrees of up to 64 individuals. Using the same algorithm the second, third, \dots , k^{th} highest likelihood pedigrees may be found by imposing additional constraints as each

*Corresponding author

high-likelihood pedigree is found (Cussens et al., 2012). It is also possible to extend the algorithm of Cowell (2009), along the lines that Tian et al. (2010) use for general Bayesian networks, to find the k highest likelihood pedigrees; however the complexity grows as $O(kn^32^n)$, thus limiting k to a relatively small number.

The algorithm presented in this paper grew out of the desire to find a large set of high likelihood pedigrees, rather than a single maximum likelihood pedigree. It uses a simple procedure of selecting one pedigree at a time, and deriving from the selected pedigree a set of candidate pedigrees by a partitioning process described below. A feature of the partitioning process is that the candidate pedigrees could have a very different structure to the pedigree that they are generated from. In addition, the partitioning process in principle covers the space of all possible pedigrees on the set of individuals, without duplicating any pedigree.

The next section introduces the partitioning algorithm in the context of finding the best k -spanning trees of an undirected graph. (This is closely related to finding pedigrees in which each individual has at most one parent in the pedigree.) The pedigree search algorithm using the partitioning is presented in Section 3. The algorithm is then applied to human and animal data, and in a simulation study, in Section 4.

2. Finding the k best spanning trees of a graph

Before presenting the pedigree search algorithm, we first present a variation of the algorithm that can find the k highest weight spanning trees of an undirected graph. The algorithm is given by Sørensen and Janssens (2005) (who looked for lowest weight spanning trees, rather than highest weight spanning trees). Suppose that we are given an undirected connected graph on n vertices, in which each edge between a pair of vertices is given a non-negative weight value. A spanning tree is a connected subgraph containing all n vertices and $n - 1$ edges, but does not have a cycle. The weight of the spanning tree is the sum of the weights of the edges of the spanning tree. The problem is to find a set of k spanning trees such that no other spanning tree has a weight greater than any spanning tree in the set of the k spanning trees.

A well known algorithm for finding the highest scoring spanning tree is Kruskal's algorithm (Kruskal, 1956), which we describe as follows. Let the nodes of a graph G be labelled by the integers from 1 to n . We form an ordered list L of the E edges, which are sorted in order of decreasing weight, with the first entry denoted by $L(1)$, the second by $L(2)$, ... , up to $L(E)$. The algorithm starts with an initial graph \mathcal{F} having no edges between the n nodes. The algorithm is simply to work through the weight-ordered edges in L , adding an edge to \mathcal{F} if in doing so it does not create a cycle, until \mathcal{F} is fully connected. It is illustrated in Algorithm 1.

Note that the first edge in the list is always added (because it cannot form a cycle by itself). Suppose that the maximum weight spanning tree \mathcal{F}^1 is made up of edges that have the increasing sequence of index values

input : An undirected edge-weighted graph G in n vertices;
a list L of the E edges of G sorted in decreasing weight;
a totally disconnected graph \mathcal{F} on the n vertices.
output: \mathcal{F} as the maximum weight spanning tree of G .

$1, \dots, n$ **Initialization**: Set $i \leftarrow 1$.

while \mathcal{F} is not connected **do**

Add edge $L(i)$ to \mathcal{F} if it does not create a cycle.

$i \leftarrow i + 1$

end

Algorithm 1: Kruskal's algorithm for finding the maximum weight spanning tree of an undirected graph

$e_1^1 (= 1), e_2^1, e_3^1, \dots, e_{n-1}^1$ of the entries in the list L . If S denotes the space of spanning trees of G , then the second highest-weight spanning tree \mathcal{F}^2 of S is the highest in $S - \mathcal{F}^1$. (Note it is possible that \mathcal{F}^1 and \mathcal{F}^2 might have the same weight.) Let us denote the list L edge indices of \mathcal{F}^2 by $e_1^2, e_2^2, e_3^2, \dots, e_{n-1}^2$. Now because \mathcal{F}^1 and \mathcal{F}^2 are distinct trees, they must differ in at least one edge. Therefore (exactly) one of the following $n - 1$ conditions must be true:

$$e_1^2 > e_1^1 \quad (1a)$$

$$e_1^2 = e_1^1 \ \& \ e_2^2 > e_2^1 \quad (1b)$$

$$e_1^2 = e_1^1 \ \& \ e_2^2 = e_2^1 \ \& \ e_3^2 > e_3^1 \quad (1c)$$

$$\vdots$$

$$e_1^2 = e_1^1 \ \& \ e_2^2 = e_2^1 \ \& \ \dots \ \& \ e_{n-2}^2 = e_{n-2}^1 \ \& \ e_{n-1}^2 > e_{n-1}^1 \quad (1d)$$

Hence, the procedure for finding the second highest weight spanning tree is to carry out Kruskal's algorithm $n - 1$ times, the first time excluding e_1^1 from the list L (constraint 1a), the second time including e_1^1 but excluding e_2^1 (1b), and so on. From the set of $n - 1$ trees found, pick the one having the highest weight (breaking ties arbitrarily if necessary), thus giving \mathcal{F}^2 . Now suppose that we want the third highest weight spanning tree \mathcal{F}^3 . Then it is either amongst the remaining $n - 2$ candidate trees found during the search for \mathcal{F}^2 , or it has edges with indices $e_1^3, e_2^3, e_3^3, \dots, e_{n-1}^3$ where one of the following holds to ensure it differs from \mathcal{F}^2 in at least one edge:

$$e_1^3 > e_1^2 \quad (2a)$$

$$e_1^3 = e_1^2 \ \& \ e_2^3 > e_2^2 \quad (2b)$$

$$e_1^3 = e_1^2 \ \& \ e_2^3 = e_2^2 \ \& \ e_3^3 > e_3^2 \quad (2c)$$

$$\vdots$$

$$e_1^3 = e_1^2 \ \& \ e_2^3 = e_2^2 \ \& \ \dots \ \& \ e_{n-2}^3 = e_{n-2}^2 \ \& \ e_{n-1}^3 > e_{n-1}^2 \quad (2d)$$

By applying Kruskal’s algorithm again several times, using these constraints, \mathcal{F}^3 may be identified. Note the first constraint (2a) is equivalent to removing the first e_1^2 edges from the list L , whilst for the other possible trees the search is started at the e_1^2 edge (2b - 2d). The procedure may be repeated until the desired number k of maximum weight spanning trees is found, see Sørensen and Janssens (2005) for more details and proof. Note that if the procedure is repeated with no upper bound k specified, then the algorithm will generate all possible spanning trees ordered by weight. It does not carry forever because for some trees the final edge added will be the last in the list L , and so for these the tree-search cannot be split on the last edge (2d). One can fruitfully view the partitioning as generating a binary search over the space of spanning trees, similar to but distinct from the standard depth-first search algorithm.

Sørensen and Janssens (2005) based their algorithm on one by Murty (1968) for finding the k best assignments; the latter was generalised by Lawler (1972). This idea of partitioning the search space into exclusive and exhaustive parts was also used in a probabilistic setting by Nilsson (1998) in an application to find the k highest probability configurations of discrete random variables having a joint distribution defined over a junction tree. Note that the k -th stage of the maximum-weight spanning tree algorithm gives the k -th highest weight tree. This is a consequence of the fact that Kruskal’s greedy search algorithm is optimal for returning the highest weight spanning tree. The best k combinatorial search applications cited above combine the partitioning with an *optimal* procedure (such as Kruskal’s algorithm) to find the k best-optimal configurations (of whatever combinatorial structure is being searched for). The simple idea in this paper is to use the exclusive and exhaustive partitioning procedure combined with a *greedy* rather than an *optimal* procedure to guide the search, in this paper over the space of high-likelihood pedigrees. This simple adaptation of an old algorithm appears to be novel, but quite powerful.

3. Pedigree search algorithm

3.1. Finding the local scores

We will consider the special case of learning pedigrees with complete data. This means that a parent of an individual is either in the sample, or if not the parent is unrelated to all other members in the sample. Under this assumption, the likelihood function for a given pedigree decomposes into a simple multiplicative form. A pedigree on n individuals (numbered from 1 up to n) may be represented by a directed-acyclic graph G on n nodes, in which each node represents the genotype of an individual. An arrow from node j to node i indicates that j is a parent of i . The graph has no directed cycles, to avoid an individual being their own ancestor. Each node of G has one of three possible parent configurations:

- The node has no incoming arrows. Hence the individual is a *founder* in the pedigree.

```

struct Score
{
integer child, parent1, parent2;
real value;
}

```

Figure 1: **Score** data structure used for storing in **value** the log-likelihood of an individual's genotype given the genotypes of the specified parents. Note that both **parent1** and **parent2** being zero, corresponds to the score if **child** is a founder.

- The node has one incoming arrow. Hence the individual has only one parent specified in the pedigree.
- The node has two incoming arrows. Hence both parents of the individual are in the pedigree.

Let g_i represent the genotype of the i -th individual. Then we let $p(g_i|g_j, g_k)$ denote the conditional probability that individual i will have genotype g_i given that it has the two parents j and k in the pedigree G having genotypes g_j and g_k respectively. If i has only one specified parent, say j then it has conditional probability $p(g_i|g_j)$, and if no parents then probability $p(g_i)$. If we let g_{π_i} denote the genotypes of the parents π_i of i in the sample, then the log-likelihood of a pedigree having parent-sets $\{\pi_i | i = 1, \dots, n\}$ decomposes into the additive form:

$$l(G) = \sum_{i=1}^n \log p(g_i | g_{\pi_i}). \quad (3)$$

The pedigree search algorithm requires the evaluation of every possible $p(g_i | g_{\pi_i})$ term, but this is carried out only once. If the markers are independent, then each $p(g_i | \pi_i)$ term is itself a product of terms one for each marker m :

$$p(g_i | g_{\pi_i}) = \prod_m p(g_i^m | g_{\pi_i}^m).$$

This decomposable form of the overall log-likelihood into *local score* contributions is used in the pedigree search algorithm. Like the spanning tree algorithm, a sorted list is formed. In this case the elements of the list are the local scores $\log p(g_i | g_{\pi_i})$ together with the child node i and the parent-set π_i of i . We store them in the following **Score** data structure, shown in Figure 1. If **S** is a instance of a score, then **S.child** gives the index $\in \{1, \dots, n\}$ of the child individual, and so on. The algorithm for making the list of local scores is outlined in Algorithm 2.

We now introduce a structure **Pedigree**. This is a directed graph with n nodes, one for each individual, which are labelled by the integers 1 up to n . Initially the pedigree is initialized to one in which there are no specified parent-sets for any of the n individuals. Note that this is slightly more than saying that there are no edges in the graph of the pedigree, as this could signify a

input : A set of n individuals and their genotypes $\{g_i : i = 1, \dots, n\}$
output: A sorted list L of $|L|$ local scores.
initialization: Set $L \leftarrow \emptyset$.;

```

for each  $i \in 1, \dots, n$  do
  for each possible parent-set  $\pi$  of  $i$  having genotype  $g_{\pi_i}$  do
    if  $p(g_i | g_{\pi_i}) > 0$  then
      Add a Score instance S to the list  $L$  where:
      S.child =  $i$ ;
      S.parent1 and S.parent2 store the indices of the
      possible parents  $\pi_i$ , (either or both may take the value zero);
      S.value =  $\log p(g_i | g_{\pi_i})$ .
    end
  end
end
  
```

Sort the list L of scores by decreasing order of their values.

Algorithm 2: Making the local scores list

pedigree in which every is a founder. Instead in the pedigree we store for each individual a boolean variable to indicate whether the individual's parent-set has been specified. It is initially set to **False** for every individual, and it is set to **True** when an individual's parent-set has been specified — this could include the case that the individual is specified to be a founder.

A pedigree is built up by adding parent-sets to each individual, with one parent-set per individual, and a pedigree is fully specified when all parent-sets have been specified. However the process of attempting to add a parent-set of an individual might make an invalid pedigree in by introducing a directed cycle in the pedigree graph. We introduce a function **AddParents(Pedigree P, Score S)** that takes as inputs a current partially specified **Pedigree P** and a **Score S**. If the **Score** structure **S** has a child value **S.child** that has already had **S.child**'s parent-set specified in **P** then the function returns **False**. Otherwise if the parent-set specified by **S.parent1** and **S.parent2**, can be made parents of **S.child** without creating a cycle, then the function modifies **P** by adding these individuals as parents of **S.child** (by adding a directed edge **S.parent1**→**S.child** if **S.parent1** > 0, and a directed edge **S.parent2**→**S.child** if **S.parent2** > 0) and returns **True**; if however adding them as parents would create a directed cycle then the function returns **False** without modifying **P**.

3.2. Making a single pedigree from the local scores

We can now present a simple greedy algorithm for making a pedigree, shown in Algorithm 3. Suppose that the local scores stored in the list L are numbered sequentially from 1 up to $|L|$, with the i -th score denoted by $L(i)$. The algorithm goes through the scores in the list in turn, trying to add a parent configuration for a child, until it has done this successfully for every child without creating a cycle. It is greedy, because at each stage it tries to add the child-parent

configuration from the local-scores list that is as high as possible. However the pedigree it makes will not necessarily achieve the maximum possible likelihood (unlike the situation for Kruskal’s algorithm). Each time a parent-set is specified in the pedigree as it is being built up, it increments a counter C that counts the number of parent-sets that have been specified. It stops when $C = n$, which occurs when every individual has had their parent-set specified. Note that the list L will always contains the scores for every individual in which they are founders (corresponding to $\pi_i = \emptyset$ for each i), thus a valid pedigree is always returned. Note also that the log-likelihood associated with the pedigree is the sum of the values of the scores for which adding parent-sets was successful. We assume that this total log-likelihood is stored in the pedigree in the quantity `value`.

input : The sorted list L of local scores.

output: A valid pedigree over the n individuals.

initialization:

A Pedigree P of n individuals with specified no parent-sets.

$P.value \leftarrow 0$

An integer $C \leftarrow 0$

```

for  $i$  from 1 to  $|L|$  do
  if  $AddParent(P, L(i))$  is true then
     $C \leftarrow C + 1$ ;
     $P.value \leftarrow P.value + L(i).value$ ;
  end
  if  $C = n$  then
    STOP and return  $P$ .
  end
end

```

Algorithm 3: `MakePedigree(L)`: Making a pedigree from a list L of ordered local scores.

3.3. The pedigree greedy search algorithm

We now combine the pedigree construction algorithm of Algorithm 3 with the partitioning algorithm, to carry out a greedy search over the space of possible pedigrees, giving two variants of the algorithm, which we shall call **Variant 1** and **Variant 2**. Note that in forming a pedigree using Algorithm 3, n scores from the list L were used, one for each individual parent-set specification. We can store the list-indices of these scores in an integer array or vector of size n in the pedigree. Let us call this array `index`, with $P.index[i]$ denoting the index in the list L of the i -th parent-set successfully added to the pedigree P . That is, the i -th parent-set added to the pedigree is from the score $L(P.index[i])$ in the list. In each pedigree we also store an integer value called `fixed`, the purpose of which is to prevent a pedigree being generated more than once by the algorithm. Before giving the general algorithm, we illustrate it in action in finding the first three pedigrees.

We make the first pedigree P^1 with Algorithm 3. Suppose P^1 has been made with the scores having the indices in the list L given by $e_1^1 (= 1), e_2^1, e_3^1, \dots, e_n^1$, which are stored in the array **index** in P^1 denoted by $P^1.\text{index}$. Hence for this pedigree $P^1.\text{index}[i] = e_i^1$, and we set $P^1.\text{fixed} = 1$. The next stage is to make the set of candidate pedigrees, one from each of the following constraints:

$$e_1^2 > e_1^1 \quad (4a)$$

$$e_1^2 = e_1^1 \ \& \ e_2^2 > e_2^1 \quad (4b)$$

$$e_1^2 = e_1^1 \ \& \ e_2^2 = e_2^1 \ \& \ e_3^2 > e_3^1 \quad (4c)$$

$$\vdots$$

$$e_1^2 = e_1^1 \ \& \ e_2^2 = e_2^1 \ \& \ \dots \ \& \ e_{n-1}^2 = e_{n-1}^1 \ \& \ e_n^2 > e_n^1 \quad (4d)$$

A pedigree made with the first constraint (4a) may be made by applying Algorithm 3 using the list L , but starting the i iteration from $e_1^1 + 1$ instead of e_1^1 . A pedigree made from the second constraint (4b) may be made by adding the parent-set associated with score $L(e_1^1)$, and completed by running for iterative loop of Algorithm 3 from $i = e_2^1 + 1$. In general the pedigree made from the j -th constraint is made by creating a pedigree that adds the parent-sets of the scores $L(e_1^1), L(e_2^1), \dots, L(e_{j-1}^1)$ used in making P^1 , and continuing the i loop from $i = e_j^1 + 1$. For the pedigree made with the j -th constraint we store in its **fixed** value the integer j .

In **Variant 1** of the algorithm, each of these pedigrees is inserted into a priority queue **Queue** that automatically keeps the pedigrees in their order of decreasing (or more accurately, non-increasing) log-likelihood. When all candidate pedigrees have been made, the pedigree at the front of the queue will be pedigree P^2 , and may be removed.

The pedigree P^3 is made by making a new set of pedigrees from P^2 and inserting them into **Queue**. P^3 will then be at the front of **Queue**. To generate the set of pedigrees from P^2 we apply one of the following constraints, which uses the **fixed** value stored in P^2 when it was formed. Let $f = P^2.\text{fixed}$. Then the constraints are:

$$\begin{aligned} e_1^3 &= e_1^2 \ \& \ e_2^3 = e_2^2 \ \& \ \dots \ \& \ e_{f-1}^3 = e_{f-1}^2 \ \& \ e_f^3 > e_f^2 \\ e_1^3 &= e_1^2 \ \& \ e_2^3 = e_2^2 \ \& \ \dots \ \& \ e_f^3 = e_f^2 \ \& \ e_{f+1}^3 > e_{f+1}^2 \\ &\vdots \\ e_1^3 &= e_1^2 \ \& \ e_2^3 = e_2^2 \ \& \ \dots \ \& \ e_{n-1}^3 = e_{n-1}^2 \ \& \ e_n^3 > e_n^2 \end{aligned} \quad (5)$$

The reason for not looking at pedigrees with constraints such as, for example,

$$e_1^3 = e_1^2 \ \& \ e_2^3 = e_2^2 \ \& \ \dots \ \& \ e_{f-2}^3 = e_{f-2}^2 \ \& \ e_{f-1}^3 > e_{f-1}^2$$

is that this constraint is equivalent to

$$e_1^3 = e_1^1 \ \& \ e_2^3 = e_2^1 \ \& \ \dots \ \& \ e_{f-2}^3 = e_{f-2}^1 \ \& \ e_{f-1}^2 > e_{f-1}^1$$

which was the constraint applied to find P^2 from P^1 . Similarly, the other constraints corresponding to some candidate pedigree generated from P^1 and already in **Queue**. This is the reason for introducing the **fixed** value for each pedigree, it prevents a pedigree from being generated more than once.

We are now ready to give the greedy pedigree search algorithm, which is laid out in Algorithm 4. The pedigree found at stage k is be stored in a list **PedList**, which is a first-in-first-out list. Intermediate pedigrees are stored in **Queue** which initially is empty. We suppose that we wish to continue the search until there are K pedigrees in **PedList**. (Note that these will not necessarily be the K highest likelihood pedigrees.) Note that if the condition ($k < K - 1$) is removed, then the algorithm will generate all possible pedigrees that can be formed out of selection of the n parent-sets from the set of local scores, that is, it does an exhaustive generation of possible (positive likelihood) pedigrees.

In **Variant 2** of the algorithm, we simply make **Queue** to be a first-in-first-out queue instead of a priority queue. As we shall see this can perform well. **Variant 3** will be introduced in Section 4.

3.4. Special case: Single parent pedigrees

Suppose that in forming the list L of local scores, we do not include any scores in which an individual has two parents, so the local scores are only for individuals that are founders or have one parent amongst the n individuals. Then Algorithm 3 is equivalent to Kruskal's search algorithm and **Variant 1** of Algorithm 4 is essentially that of Sørensen and Janssens (2005), but instead of generating undirected maximum spanning weight trees in the order of decreasing weight, it generates pedigrees in order of decreasing likelihood, in which no individual has more than one parent. One minor difference it that topologically, each such pedigree need not be connected, so graphically the pedigree could be a forest of directed trees rather than a single connected tree. This arises because the local scores contain terms in which individuals are founders; in contrast in the spanning tree algorithm the weights are only ever between edges of pairs of nodes.

3.5. Bounding the greedy search algorithm

As mentioned in Section 3.3, removing the condition $k < K - 1$ from the **while** loop of Algorithm4 means that all possible (positive likelihood) pedigrees will be generated by the algorithm. If the number of individuals is small, then this exhaustive generation may be possible and the maximum likelihood pedigree may be identified, in fact all pedigrees may be enumerated. For the Romanov example involving 9 individuals (see Section 4.1), it turns out that there are 11512 possible pedigrees which give consistent genotype parent-child combinations (using sex-information). For many individuals the search space may be too large for an exhaustive enumeration to be computationally feasible.

input : The sorted list L of local scores;
 A queue **Queue** of candidate pedigrees, initially empty;
 PedList of found pedigrees, initially empty.

initialization:

Pedigree $P = \text{MakePedigree}(L)$;
 $P.\text{fixed} = 1$;
 Insert P into **Queue**;
 $k \leftarrow 0$.

search iterations:

while *Queue is not empty and $k < K - 1$* **do**
 $k \leftarrow k + 1$;
 Remove the first pedigree from **Queue**, call it P^k ;
 Insert P^k to **PedList**.
 for i from $P^k.\text{fixed}$ until n **do**
 Make new initialized **Pedigree** P ;
 $C \leftarrow 0$;
 for j from 1 to $P^k.\text{fixed} - 1$ **do**
 AddParent($P, L(P^k.\text{index}[j])$);
 $C \leftarrow C + 1$;
 end
 $P.\text{fixed} \leftarrow i$;
 for j from $P^k.\text{fixed} + 1$ until $|L|$ **do**
 if AddParent($P, L(j)$) is true **then**
 $C \leftarrow C + 1$;
 $P.\text{value} \leftarrow P.\text{value} + L(i).\text{value}$;
 end
 end
 if $C = n$ **then**
 Insert P into **Queue**
 else
 Discard P
 end
 end
end
 $k \leftarrow k + 1$;
 Remove the first pedigree from **Queue**, call it P^k ;
 Insert P^k into **PedList**.

Algorithm 4: Greedy pedigree search to find K high-likelihood pedigrees. In **Variant 1** of the algorithm, **Queue** is a priority queue, with highest likelihood pedigrees at the front, whereas in **Variant 2**, **Queue** is a first-in-first-out queue, so that pedigrees are inserted at the back and removed from the front.

However it is possible to introduce a bounding condition so that for not too many individuals the algorithm terminates in reasonable time and the maximum likelihood pedigree is thus identified. The modification of Algorithm 4 to achieve this is straightforward, and is as follows.

Consider the state of the pedigree P formed from P^k after the first of the inner j -loops. This will be in a state in which the parent-sets of C individuals have been specified, which means that there are a further $n - C$ individuals' parent-sets to specify. We also have the log-likelihood of the pedigree contributed by the C individuals stored in $P.value$. So if we now add up the highest score of each of the $n - C$ individuals in the list from the scores located from position $1 + P^k.index[P^k.fixed]$ up to $|L|$, and add this total to $P.value$, we will get an upper bound of the log-likelihood of any possible pedigree completion of P . If this is lower than the log-likelihood of the current best pedigree (which value is kept track of during the execution of the algorithm) then we may discard P , and not add it or any completion to $Queue$. Hence some potentially large sections of the pedigree search space can be disregarded as they are irrelevant to finding the highest likelihood pedigree.

4. Computer evaluations

Here is a summary of computer evaluations of the performance of the algorithm. All computations were carried out using a computer with an AMD dual-core 1.96GHz processor and 7GB of ram running the Debian 6 (squeeze) Linux operating system. In all evaluations Hardy-Weinberg equilibrium was assumed.

4.1. Romanov data

In July 1991, in a shallow grave 20 miles from Ekaterinburg, Russia, nine skeletons were found, some of which were believed to be the remains of Tsar Nicholas II, his wife, three of their five children. This was confirmed in careful DNA analysis by (Gill et al., 1994). Table 4.1 shows STR genotype data for the nine skeletons and their designated identification as given in (Gill et al., 1994).

Skeleton	HUMVWA/31	HUMTHO1	HUMF12A1	HUMFES/FPS
1 (servant)	14,20	9,10	6,16	10,11
2 (doctor)	17,17	6,10	5,7	10,11
3 (child)	15,16	8,10	5,7	12,13
4 (Tsar)	15,16	7,10	7,7	12,12
5 (child)	15,16	7,8	3,7	12,13
6 (child)	15,16	8,10	3,7	12,13
7 (Tsarina)	15,16	8,8	3,5	12,13
8 (servant)	15,17	6,9	5,7	8,10
9 (servant)	16,17	6,6	6,7	11,12

Table 1: Romanov STR data

Variant 1 of Algorithm 4 was run with no upper bound K of the number of iterations of the **while** loop, and without the bounding procedure described in Section 3.5, so that all possible pedigrees were generated. (In the absence of suitable population allele frequencies, each marker was assumed to consist of eight alleles, (inclusive of the ones in the table), with a uniform distribution.) As mentioned above there are 11512 possible pedigrees (using sex information). The top-left plot in Figure 2 shows the log-likelihoods of the pedigrees in the order that they were added to the **PedList**, (that is $P^1, P^2, \dots, P^{11512}$). The highest likelihood pedigree was P^2 . We see from the plot that there is generally a steady decrease in the log-likelihood but with occasional increases, and that many of the pedigrees have log-likelihoods much lower than the highest value. The likelihood of the most likely pedigree is 1.81×10^{-39} , which amounts to approximately 10% of the sum of the likelihoods at 1.71×10^{-38} . The first 254 pedigrees account for 95% of the total likelihood of all the pedigrees, the first 266 for 99% of the total. The top-left plot of Figure 2 shows the cumulative sum of likelihoods of the first k pedigrees found as a ratio to the sum of the likelihoods of all 11512 pedigrees, plotted for k values up to 300. Equivalent plots for **Variant 2** are shown on the bottom panel of Figure 2 for which: the first 254 pedigree account of 78.3% of the total likelihood, the 95% level is reached on pedigree 513, and the 99% level at pedigree 863. We see that for this dataset **Variant 1** is being more efficient at picking out the higher likelihood pedigrees.

4.2. Simulation with a known pedigree of 20 individuals

A simulation study was carried out using the highly inbred pedigree of twenty individuals taken from (Cowell, 2009), shown in Figure 3. In each of one thousand simulations, genotypes were simulated for all the individuals consistent with parentage assignments in the pedigree, the maximum likelihood pedigree was found using the algorithm described in (Cowell, 2009), using sex information, and the log-likelihood was recorded. Algorithm 4 was also run, either until it found a pedigree having the maximum likelihood, or $K = 5$ million pedigrees were put in the **PedList**. The bounding described in Section 3.5 was not employed in the search. The iteration of the highest likelihood pedigree found by the greedy search algorithm was recorded, together with the log-likelihood achieved. The log-likelihood of the generating pedigree was also recorded. The results from **Variant 1** and **Variant 2** for the same generated genotypes are markedly different.

Variant 1

For 255 of the runs, the first pedigree was the highest likelihood pedigree, for 285 runs it was the second, and for 106 the third. In 759 runs, the highest likelihood pedigree was amongst the first 20 pedigrees found. However, in 70 of the runs, more than 10,000 iterations were required before finding the highest. In addition, in 16 of the 1000 runs, the algorithm did not find the highest likelihood pedigree within the 5 million iteration limit set. Figure 4 shows the

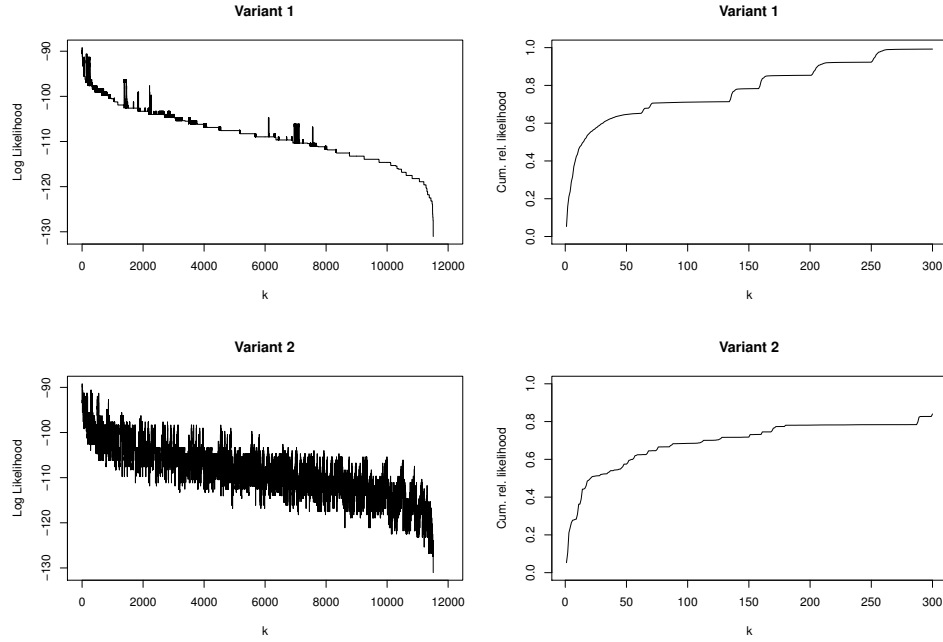


Figure 2: Log-likelihoods of pedigrees found from the Romanov data of nine individuals, in the order found. Top left: all 11512 pedigrees using **Variant 1**, top right, the normalized cumulative likelihoods to the first 300 pedigrees, using **Variant 1**. Bottom row: as for top row but with **Variant 2** of Algorithm 4.

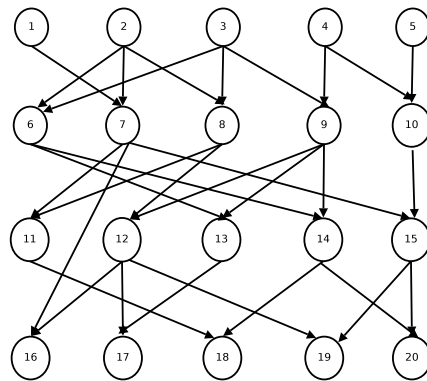


Figure 3: An inbred pedigree of twenty individuals.

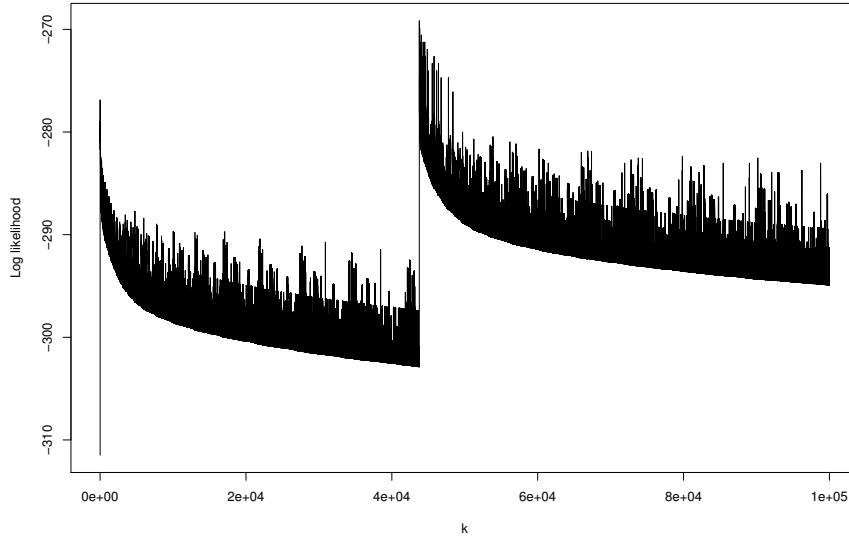


Figure 4: The log-likelihoods of the first 100,000 pedigrees, where the maximum occurred at iteration 43769.

log-likelihoods of the first 100,000 pedigrees found by the search algorithm for a run in which the maximum was found on iteration 43769. Note that until the jump to this pedigree, the plot gives the impression that the highest likelihood pedigree has been found on the second iteration. Although such trace plots can be suggestive that a maximum likelihood has been found, they can be misleading as this example shows. From the runs that did find the highest likelihood pedigree, the greatest number of iterations taken to do so was 3473461.

Note that in all of these runs the bounding strategy described in Section 3.5 was not used, so that the greedy algorithm did not identify the true maximum. The example from Figure 4 was re-run using the bounding technique. The computation took used 28587 iterations altogether for a complete search of pedigree space, with the highest likelihood pedigree found on iteration 9198.

Algorithm 4 with the bounding strategy was also re-run on each of the 16 pedigrees for which the algorithm without bounding failed to find the maximum pedigree after 5 million iterations. A limit was again set to 5 million iterations. In 14 out of the 16 runs, the highest likelihood pedigree was found, with three requiring over 1 million iterations.

Variant 2

The same sets of genotypes for the 1000 simulations for **Variant 1** were used for **Variant 2** analyses, initially without using the bounding. For 255 of the runs, the first pedigree was the highest likelihood pedigree, (the same as for **Variant 1** as it should be because they both start with the same first

greedily selected pedigree). For 285 runs it was the second. For the remainder of the runs, there is a gap until the 9-th iteration to finding the highest likelihood pedigree. In 908 runs the highest pedigree was found within 1000 iterations, rising to 972 runs for up to 10000 iterations, and 994 for 100000 iterations. Of the remaining six pedigrees, five took from 104222 to 342247 iterations to find the highest pedigree, the remaining one took 7830717 iterations. In contrast, using **Variant 1** the latter was found in in 541093 iterations.

However when **Variant 2** of the algorithm was used with bounding, *all* runs found the highest likelihood pedigree, the longest run taking 32427 iterations, the next longest 14321 iterations.

Variant 3

In many pedigree search algorithms, such as those based on backtracking or MCMC search, the search procedure moves around pedigree space making small local changes to pedigrees, such as adding a parent, removing a parent, or reversing the rôle of parent and child relationship, so that successive pedigrees are very close in structure, differing in one or two edges. Such algorithms can spend a lot of time searching a poor part of pedigree space, or even getting trapped at a local maximum. The motivation behind Algorithm 4 is that the pedigrees produced by the partitioning would be well spread out in pedigree space, so that two such pedigrees can differ dramatically in structure. This it is hoped would make the search range widely over pedigree space. For **Variant 1** the focus is always on the currently best partition found. This appears to do well as show in the Figure 2. However, Figure 4 shows that **Variant 1** is not immune from the problems of getting stuck for a long time in the vicinity of a local maximum. **Variant 2** of Algorithm 4 is akin to a breadth-first search amongst the partitions, so that the successive pedigrees being found are located far apart in pedigree space in terms of their structural differences. This appears to be better than **Variant 1**, in that it is more successful in finding the highest pedigree, though the number of iterations required has a long tail, with six pedigrees requiring more than 100,000 iterations, without bounding, but drastically reduced with bounding. However it does not have the greedy focus of **Variant 1** in choosing the order in which pedigrees are examined.

The motivation behind **Variant 3** is to combine aspects of both of these searches into one that is more greedy than **Variant 2** but less than **Variant 1**. The idea is simple: Algorithm 4 is run as **Variant 2** using the first-in-first-out **Queue**, but periodically after a fixed number of iterations has been performed, **Queue** is sorted so that the highest likelihood pedigrees are at the front of the list.

The five pedigrees that took more than 10000 iterations to find the highest pedigree using the **Variant 2** with bounding were selected and this extra periodic sorting step was applied, both with and without bounding. Sorting was carried out every 10000 iterations (which meant that for the first 10000 iterations the algorithm behaves the same as **Variant 2**). The number of iterations in each case are laid out in Table 4.2, which also includes analyses using **Variant 1** with and without bounding, and **Variant 2** without bounding. It

would seem that **Variant 3** performs best, however the application of bounding has a mixed response. In addition, the performance does depend upon the period used between sorts, as illustrated in the last row in the table. Note that for the **Variant 3** runs, the pedigree is marked as found when it is removed from **Queue** rather than when it is put into **Queue**, which is the reason why several of the values in the table are 1 above a multiple of 1000 or 10000.

Algorithm	Pedigree				
	1	2	3	4	5
Variant 1 no bound	NF	1441427	NF	541093	129209
Variant 1 with bound	665086	225180	73866	12639	28726
Variant 2 no bounding	246622	95589	198140	NF	106065
Variant 2 with bounding	32427	14321	13525	10684	13413
Variant 3 no bounding	30001	20001	30002	60003	20001
Variant 3 with bounding	20001	10001	10002	10003	10001
Variant 3 with bounding*	4001	3001	4002	15003	3001

Table 2: Comparison of of iterations required by some some selected pedigrees to find highest pedigree, NF denotes not found within 5 million iterations. *Bottom row: period between sorts 1000 iterations.

4.3. Data for shrimp

The third example we look at is a two generation dataset of the black tiger shrimp *P. monodon* (Jerry et al., 2005), downloaded from the FRANz software web site (Riester et al., 2009). The dataset from the website has profiles for 85 individual shrimp on seven loci. However for 10 shrimp the profiles are incomplete on some markers, and so these individuals were removed, leaving a dataset of 75 individuals. The FRANz software was used to generate estimates of allele frequencies. The three variants of Algorithm 4 were carried out to 100,000 iterations. (Curiously the same results were identical for with and without bounding, which might be because there are many pedigree having a likelihood close to the maximum, or perhaps simply because there are more individuals in this example compared to the others examined earlier. This is an issue that requires further exploration.) The trace plots are shown in Figure 5. Both **Variant 1** and **Variant 3** found 192 pedigrees having the highest likelihood value of -1084.44, whilst **Variant 2** found 3 such pedigrees. The next highest likelihood value found was -1085.14; this was found by **Variant 1** for 480 pedigrees and by **Variant 3** for 568 pedigrees, but for only 12 pedigrees by **Variant 2**. Extending the number of iterations to 500,000 no additional pedigrees having log-likelihood of -1084.44 were found by either **Variant 1** or **Variant 3**, however the number of pedigrees found having a log-likelihood of -1085.14 rose to 2856 for **Variant 1** and to 2824 for **Variant 3**.

The same dataset was analysed in 100 runs of the FRANz software, which implements the simulated annealing algorithm of Almudevar (2003) for finding the maximum likelihood pedigree. In these 100 runs, 72 found a pedigree of highest log-likelihood of -1084.44, the remaining 28 found a pedigree having

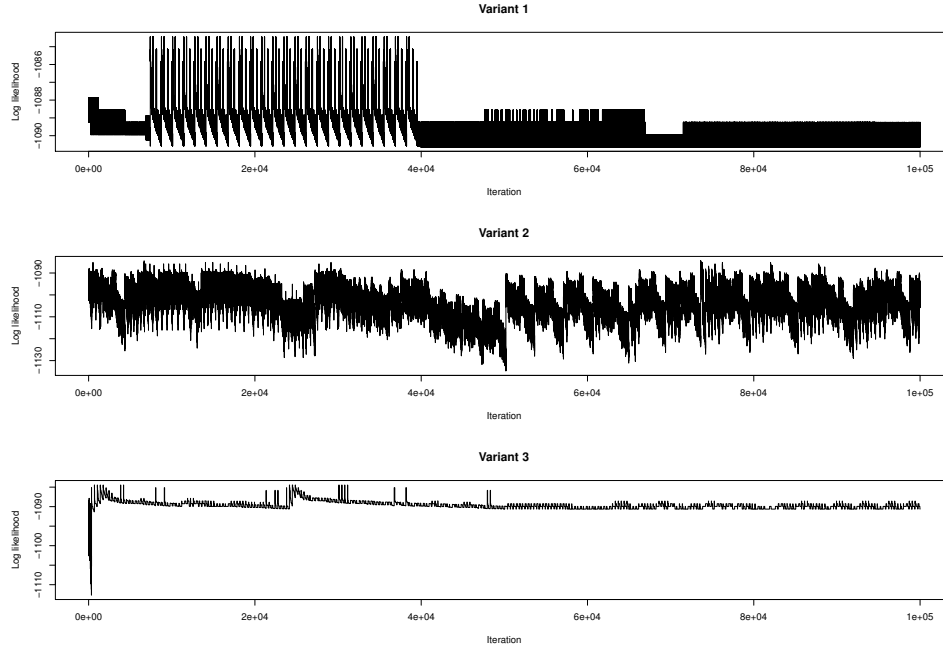


Figure 5: Successive pedigree log-likelihoods over 100,000 iterations, found for 75 individual black tiger shrimp using all algorithm variants, with **Variant 3** having a sort period of 350 iterations. Note the different scales on the likelihood axis.

highest log-likelihood of -1085.14. (By way of a timing comparison, each of the FRANz runs took approximately 3 seconds, whilst 100,000 iterations of the search algorithm took approximately 66 seconds on the same computer.)

As we can see from Figure 5, the decay in the log-likelihood values is quite slow and not like the sharp decay exhibited in Figure 2. The cumulative relative likelihood of the pedigrees found by **Variant 3** of Figure 5, is plotted in Figure 6 where the likelihoods have been sorted from highest to lowest. Note that this is cumulative relative to the set of pedigrees found, not to the total likelihood of all possible pedigrees. The highest 1951 pedigrees found account for 50% of the total likelihood, the number rising to 69834 pedigrees to account for 95% of the total likelihood found.

5. Summary

This paper has presented a simple greedy algorithm for finding a large number of high-likelihood pedigrees, and illustrated it with two datasets and a simulation study. The algorithm generates candidate pedigrees by a partitioning of the pedigree search space, where the partitioning at any stage depends upon the current pedigree under consideration. A characteristic of the partitioning is

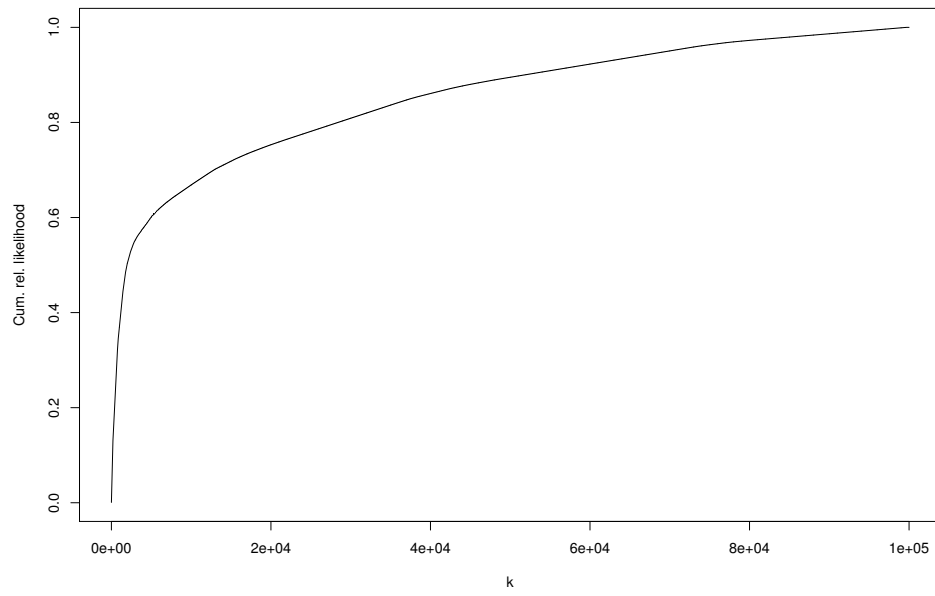


Figure 6: The cumulative relative likelihoods of the 100,000 pedigrees found by **Variant 3** in Figure 5, where the pedigrees have been sorted in order of decreasing likelihood.

that pedigrees considered consecutively can have very different graphical structure. This helps the search procedure to make large jumps in the pedigree space. In principle the algorithm generates all possible (positive likelihood) pedigrees without duplication, but in practice the space of pedigrees will usually be too large for an exhaustive search to be carried out.

Three variants of the algorithm were presented. In **Variant 1** a priority queue is used to store the candidate pedigrees, and on each iteration the highest likelihood candidate pedigree is selected from the queue. This generally performs quite well, but as illustrated in Figure 4 can take many iterations before finding a maximum likelihood pedigree. In **Variant 2** the candidate pedigrees are stored in a first-in-first-out queue, which means that a wider variety of partitions is explored. This appears to be more efficient at finding a highest likelihood pedigree quite early, however there is wide variability in the likelihoods of pedigrees in successive iterations. A third variant was also examined, in which candidate pedigrees are stored in a first-in-first-out queue, but periodically the queue is sorted so that high-likelihood pedigrees are at the front of the queue. Note that if the sorting period is set to 1, then this reduces to **Variant 1**, and if the sorting period is set to be larger than the pre-set number of iterations to be carried out, then this reduces to **Variant 2**. This seemed to perform the best, though the behaviour will depend on the choice of sorting period. It is planned to explore this issue further elsewhere. A bounding procedure was described, but it appears this might be effective only for a low number of individuals; again this is an issue that will be explored elsewhere.

There are various extensions that could be considered. One is to use the set of pedigrees found during a search in a pedigree averaging procedure. Indeed, this was the main motivation for developing the algorithm. Although a maximum likelihood pedigree will contain many features in common with the true pedigree, averaging over a set of high-likelihood pedigrees will take account of pedigree uncertainty. For example one could look at how often a particular feature in a pedigree, for example a particular individual i has a particular parent j , and using the pedigree likelihoods find the posterior probability of such a parent child combination (assuming, say, a uniform prior over the two possibilities of j is a parent of i , and j is not a parent of i).

Another possibility is to incorporate structural prior information into the set of high likelihood pedigrees found. Examples of structural priors are proposed by Egeland et al. (2000), Sheehan and Egeland (2007) and Almudevar and LaCombe (2012). When structural priors are such that they decompose locally into simple factors in the same manner as the log-likelihood (3) then incorporation into a search procedure may be relatively straightforward. However not all structural priors are of this amenable form. For example, we might wish to exclude pedigrees in which a pair of parents has more than a certain number of offspring, or to put a prior on the number of offspring a pair of individuals can have. Or we might like to exclude two individuals that are separated by more than a certain number of generations from mating, or put a prior on inter-generational mating. These constraints, whether hard or soft, could be quite difficult and/or computationally expensive to incorporate into some types of

search algorithms. However, such structural priors could be straightforwardly combined with the set of pedigrees found after the likelihood based search procedure of this paper. Alternatively, and probably better, candidate pedigrees could be found using the likelihood search of Algorithm 4, and then combined with structural prior information (and so adjusting the `P.value` score) before being placed in `Queue`. In this way the search will be more focussed on the high posterior pedigrees of interest rather than high likelihood pedigrees; this is an area for further research.

References

- Almudevar, A., 2003. A simulated annealing algorithm for maximum likelihood pedigree reconstruction. *Theoretical Population Biology* 63, 63–75.
- Almudevar, A., LaCombe, J., 2012. On the choice of prior density for the Bayesian analysis of pedigree structure. *Theoretical Population Biology* 81, 131–143.
- Blouin, M. S., 2003. DNA-based methods for pedigree reconstruction and kinship analysis in natural populations. *TRENDS in Ecology and Evolution* 18 (10), 503–511.
- Cowell, R. G., 2009. Efficient maximum likelihood pedigree reconstruction. *Theoretical Population Biology* 76, 285–291.
- Cussens, J., 2010. Maximum likelihood pedigree reconstruction using integer programming. In: *In Proceedings of the Workshop on Constraint Based Methods for Bioinformatics (WCB-10)* Edinburgh.
- Cussens, J., Bartlett, M., Jones, E. M., Sheehan, N. A., 2012. Maximum likelihood pedigree reconstruction using integer linear programming. *Genetic Epidemiology*, (submitted and under review).
- Egeland, T., Mostad, P. F., Mevåg, B., Stenersen, M., 2000. Beyond traditional paternity and identification cases: Selecting the most probable pedigree. *Forensic Science International* 110, 47–59.
- Gill, P., Ivanov, P. L., Kimpton, C., Piercy, R., Benson, N., Tully, G., Evett, I., Hagelberg, E., Sullivan, K., 1994. Identification of the remains of the Romanov family by DNA analysis. *Nature Genetics* 6, 130–135.
- Jerry, D. R., Evansa, B. S., Kenway, M., Wilson, K., 2005. Development of a microsatellite DNA parentage marker suite for black tiger shrimp *penaeus monodon*. *Aquaculture* 255, 1–4.
- Jones, A. G., Ardren, W. R., 2003. Methods of parentage analysis in natural populations. *Molecular Ecology* 12, 2511–2523.

- Kruskal, J. B., February 1956. On the shortest spanning subtree of a graph and the traveling salesman problem. *Proceedings of the American Mathematical Society* 7 (1), 48–50.
- Lawler, E., 1972. A procedure for computing the K best solutions to discrete optimization problems and its application to the shortest path. *Management Science* 7, 401–405.
- Murty, K. G., 1968. An algorithm for ranking all the assignments in order of increasing cost. *Operations Research* 16 (3), 682–687.
- Nilsson, D., June 1998. An efficient algorithm for finding the M most probable configurations in a probabilistic expert system. *Statistics and Computing* 8, 159–173.
- Pemberton, J. M., 2008. Wild pedigrees: the way forward. *Proceedings of the Royal Society, Series B* 275, 613–621.
- Riester, M., Stadler, P. F., Klemm, K., 2009. FRANz: Fast reconstruction of wild pedigrees. *Bioinformatics* 25, 2134–2139.
- Sheehan, N. A., Egeland, T., Jul 2007. Structured incorporation of prior information in relationship identification problems. *Annals of Human Genetics* 71 (Pt 4), 501–518.
URL <http://dx.doi.org/10.1111/j.1469-1809.2006.00345.x>
- Silander, T., Myllymäki, P., 2006. A simple approach to finding the globally optimal Bayesian network structure. In: Dechter, R., Richardson, T. (Eds.), *Proceedings of the 22nd Conference on Artificial intelligence (UAI 2006)*. AUAI Press, pp. 445–452.
- Sörensen, K., Janssens, G. K., 2005. An algorithm to generate all spanning trees of a graph in order of increasing cost. *Pesquisa Operacional* 25 (2), 219–229.
- Thompson, E. A., 1976. Inference of genealogical structure. *Social Science Information sur les Sciences Social* 15, 477–526.
- Thompson, E. A., 1986. *Pedigree Analysis in Human Genetics*. John Hopkins University Press, Baltimore.
- Tian, J., He, R., Ram, L., 2010. Bayesian model averaging using the k -best Bayesian network structures. In: *Proceedings of the 26th Conference on Uncertainty in Artificial Intelligence (UAI 2010)*. P. Grünwald and P. Spirtes (Editors). AUAI Press. ISBN 978-0-9749039-6-5.